

Abstract

The invention relates to method, wherein the number of repeat sequences which are present in a sample is determined by means of melting temperature analysis. More precisely, the
5 invention relates to a method for analysis of a target nucleic acid consisting of repetitive and non repetitive sequences comprising (i) hybridization of at least one polynucleotide hybridization probe comprising a first segment which is complementary to a non repetitive region and a second segment which is complementary to an adjacent repetitive region, said second segment consisting of a defined number of repeats and (ii) determination of the
10 melting point temperature of the hybrid which has been formed between the target nucleic acid and the at least one hybridization probe.